

<110> Folkesson, Anders

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<130> Complete sequence of the cs7 insert

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Asp Val Ala Gly Asn Leu Arg Trp Val Glu Thr Gly Asn Lys Leu Lys	
335 340 345	
gtg gag aac ccc acc ccg ttt tac atg aat tta gcc tct gtc aca gta	38539
Val Glu Asn Pro Thr Pro Phe Tyr Met Asn Leu Ala Ser Val Thr Val	
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Gly Gly Lys Pro Ile Thr Gly Leu Glu Tyr Val Pro Pro Phe Ala Asp	
365 370 375	
aaa aca cta aat atg cca ggt agt gcc cat ggt gat atc gag tgg aga	38635
Lys Thr Leu Asn Met Pro Gly Ser Ala His Gly Asp Ile Glu Trp Arg	
380 385 390 395	
gtt att aca gac ttt ggt ggt gaa agt cat ccg ttc cac tac gtt ctt	38683
Val Ile Thr Asp Phe Gly Gly Glu Ser His Pro Phe His Tyr Val Leu	
400 405 410	
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Lys Met Lys Phe Lys Gln Pro Ala Leu	
415 420	
cta ctg ttc atc gcg gga gtg gtt cat tgc gca aat gcg cac act tac	38784

Leu	Leu	Phe	Ile	Ala	Gly	Val	Val	His	Cys	Ala	Asn	Ala	His	Thr	Tyr	
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Thr	Phe	Asp	Ala	Ser	Met	Leu	Gly	Asp	Ala	Ala	Lys	Gly	Val	Asp	Met	
		440					445					450				
tcg	ctc	ttt	aac	cag	ggg	tta	caa	cag	cca	ggg	act	tat	cgc	gtg	gac	38880
Ser	Leu	Phe	Asn	Gln	Gly	Leu	Gln	Gln	Pro	Gly	Thr	Tyr	Arg	Val	Asp	
	455					460					465					
gtg	atg	gtg	aat	ggg	aaa	cgt	gtc	gac	acc	cgt	gat	gtg	gtg	ttc	aaa	38928
Val	Met	Val	Asn	Gly	Lys	Arg	Val	Asp	Thr	Arg	Asp	Val	Val	Phe	Lys	
470					475					480					485	
ttg	gaa	aag	gat	ggg	caa	gga	acg	cct	gtt	ctg	gct	cct	tgt	ttg	acg	38976
Leu	Glu	Lys	Asp	Gly	Gln	Gly	Thr	Pro	Val	Leu	Ala	Pro	Cys	Leu	Thr	
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gtc	agt	cag	ctt	tca	cgc	tac	ggc	gta	aaa	acg	gaa	gat	tac	cct	cag	39024
Val	Ser	Gln	Leu	Ser	Arg	Tyr	Gly	Val	Lys	Thr	Glu	Asp	Tyr	Pro	Gln	
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Leu	Trp	Lys	Ala	Ala	Lys	Pro	Pro	Asp	Glu	Cys	Ala	Asp	Leu	Thr	Ala	
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att	cca	cag	gct	aaa	gcg	gta	ctg	gat	atc	aat	aat	cag	caa	ctg	caa	39120
Ile	Pro	Gln	Ala	Lys	Ala	Val	Leu	Asp	Ile	Asn	Asn	Gln	Gln	Leu	Gln	
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ctg	agt	att	ccg	cag	ttg	gcg	ttg	cgt	ccg	gaa	ttt	aag	ggg	atc	gct	39168
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cca	gaa	gat	ctt	tgg	gat	gat	ggg	att	ccg	gcg	ttt	ctg	atg	aac	tac	39216
Pro	Glu	Asp	Leu	Trp	Asp	Asp	Gly	Ile	Pro	Ala	Phe	Leu	Met	Asn	Tyr	
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Ser	Ala	Arg	Thr	Thr	Gln	Thr	Asp	Tyr	Lys	Met	Asp	Met	Val	Gly	Arg	
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Asp	Asn	Ser	Ser	Trp	Val	Gln	Leu	Gln	Pro	Gly	Ile	Asn	Ile	Gly	Ala	
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Trp	Arg	Val	Arg	Asn	Ala	Thr	Ser	Trp	Gln	Arg	Ser	Ser	Gln	Leu	Ser	
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Phe	Asp	Ser	Val	Pro	Phe	Thr	Gly	Val	Met	Leu	Ala	Ser	Asp	Asp	Asn	

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Met	Val	Pro	Tyr	Ser	Glu	Arg	Gln	Phe	Ala	Pro	Val	Val	Arg	Gly	Ile	
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Ala	Arg	Thr	Gln	Ala	Arg	Val	Glu	Val	Lys	Gln	Asn	Gly	Tyr	Thr	Ile	
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Tyr	Asn	Thr	Thr	Val	Ala	Pro	Gly	Pro	Phe	Ala	Leu	Arg	Asp	Leu	Ser	
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Ala	Thr	His	Asn	Gln	Ala	Ala	Leu	Leu	Gly	Leu	Gly	Gly	Ser	Leu	Gly	
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cgg	tgg	ggg	agt	tta	tct	gtc	gat	gga	agc	gac	aca	cac	agt	cag	cgt	39984
Arg	Trp	Gly	Ser	Leu	Ser	Val	Asp	Gly	Ser	Asp	Thr	His	Ser	Gln	Arg	
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Gln	Gly	Glu	Ala	Val	Gln	Gln	Gly	Ala	Ser	Trp	Arg	Leu	Arg	Tyr	Ser	
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agc	tcg	cgt	act	acc	ctg	atg	ttg	agt	cag	tca	tgg	ggg	agg	cat	ttg	40224
Ser	Ser	Arg	Thr	Thr	Leu	Met	Leu	Ser	Gln	Ser	Trp	Gly	Arg	His	Leu	
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<213> *Salmonella typhimurium*

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 Leu Ile Pro Val Ser Gly Leu Lys Ala Gly Lys Asn Ala Pro Ser Ala
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 Lys Ile Ala Lys Leu Val Val Asn Ser Thr Thr Leu Lys Glu Phe Gly
 65 70 75 80
 Val Arg Gly Ile Ser Asn Asn Val Val Asp Ser Thr Gly Thr Ala Trp
 85 90 95
 Arg Val Ala Gly Lys Asn Thr Gly Lys Glu Ile Gly Val Gly Leu Ser
 100 105 110
 Ser Asp Ser Leu Arg Arg Ser Asp Ser Thr Glu Lys Trp Asn Gly Val
 115 120 125
 Asn Trp Met Thr Phe Asn Ser Asn Asp Thr Leu Asp Ile Val Leu Thr
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 <213> Salmonella typhimurium

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 Ala Gly Thr Ala Gly Ala Thr Leu Ser Val Ser Asn Pro Gln Asn Tyr
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 Pro Ile Leu Val Gln Ser Ser Val Lys Ala Ala Asp Lys Ser Ser Pro
 65 70 75 80
 Ala Pro Phe Leu Val Met Pro Pro Leu Phe Arg Leu Glu Ala Asn Gln
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 Gln Ser Gln Leu Arg Ile Val Arg Thr Gly Gly Asp Met Pro Thr Asp
 100 105 110
 Arg Glu Thr Leu Gln Trp Val Cys Ile Lys Ala Val Pro Pro Glu Asn

115 120 125
 Glu Pro Ser Asp Thr Gln Ala Lys Gly Ala Thr Leu Asp Leu Asn Leu
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 Ser Ile Asn Ala Cys Asp Lys Leu Ile Phe Arg Pro Asp Ala Val Lys
 145 150 155 160
 Gly Thr Pro Glu Asp Val Ala Gly Asn Leu Arg Trp Val Glu Thr Gly
 165 170 175
 Asn Lys Leu Lys Val Glu Asn Pro Thr Pro Phe Tyr Met Asn Leu Ala
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 Ser Val Thr Val Gly Gly Lys Pro Ile Thr Gly Leu Glu Tyr Val Pro
 195 200 205
 Pro Phe Ala Asp Lys Thr Leu Asn Met Pro Gly Ser Ala His Gly Asp
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 50 55 60
 Asp Thr Arg Asp Val Val Phe Lys Leu Glu Lys Asp Gly Gln Gly Thr
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 Pro Val Leu Ala Pro Cys Leu Thr Val Ser Gln Leu Ser Arg Tyr Gly
 85 90 95
 Val Lys Thr Glu Asp Tyr Pro Gln Leu Trp Lys Ala Ala Lys Pro Pro
 100 105 110
 Asp Glu Cys Ala Asp Leu Thr Ala Ile Pro Gln Ala Lys Ala Val Leu
 115 120 125
 Asp Ile Asn Asn Gln Gln Leu Gln Leu Ser Ile Pro Gln Leu Ala Leu
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 Arg Pro Glu Phe Lys Gly Ile Ala Pro Glu Asp Leu Trp Asp Asp Gly

145 155 160
 Ile Pro Ala Phe Leu Met Asn Tyr Ser Ala Arg Thr Thr Gln Thr Asp
 165 170 175
 Tyr Lys Met Asp Met Val Gly Arg Asp Asn Ser Ser Trp Val Gln Leu
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 Gln Pro Gly Ile Asn Ile Gly Ala Trp Arg Val Arg Asn Ala Thr Ser
 195 200 205
 Trp Gln Arg Ser Ser Gln Leu Ser Gly Lys Trp Gln Ala Ala Tyr Thr
 210 215 220
 Tyr Ala Glu Arg Gly Leu Tyr Ser Leu Lys Ser Arg Leu Thr Leu Gly
 225 230 235 240
 Gln Lys Thr Ser Gln Gly Glu Ile Phe Asp Ser Val Pro Phe Thr Gly
 245 250 255
 Val Met Leu Ala Ser Asp Asp Asn Met Val Pro Tyr Ser Glu Arg Gln
 260 265 270
 Phe Ala Pro Val Val Arg Gly Ile Ala Arg Thr Gln Ala Arg Val Glu
 275 280 285
 Val Lys Gln Asn Gly Tyr Thr Ile Tyr Asn Thr Thr Val Ala Pro Gly
 290 295 300
 Pro Phe Ala Leu Arg Asp Leu Ser Val Thr Asp Ser Ser Gly Asp Leu
 305 310 315 320
 His Val Thr Val Trp Glu Ala Asp Gly Ser Thr Gln Met Phe Val Val
 325 330 335
 Pro Tyr Gln Thr Pro Ala Ile Ala Leu His Gln Gly Tyr Leu Lys Tyr
 340 345 350
 Ser Leu Leu Ala Gly Arg Tyr Arg Ser Ser Asp Ser Ala Thr Asp Lys
 355 360 365
 Arg Gln Ile Ala Gln Ala Thr Leu Met Tyr Gly Leu Pro Trp Asn Leu
 370 375 380
 Thr Ala Tyr Gly Gly Ile Gln Ser Ala Thr His Asn Gln Ala Ala Leu
 385 390 395 400
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 405 410 415
 Gly Ser Asp Thr His Ser Gln Arg Gln Gly Glu Ala Val Gln Gln Gly
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 Ala Ser Trp Arg Leu Arg Tyr Ser Asn Gln Leu Thr Ala Thr Gly Thr
 435 440 445
 Asn Phe Phe Leu Thr Arg Trp Gln Tyr Ala Ser Gln Gly Tyr Asn Thr
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 Arg Thr Asp Trp Arg Asn Arg Pro Gly His Asp Asp Ser Tyr Gly Leu
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 530 535 540
 Gln Asn Arg Thr Leu Trp Arg Asn Gly Ala His Arg Lys Glu Asn Ile
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 Thr Ser Leu Trp Phe Ser Met Pro Leu Ser Arg Trp Thr Gly Asn Asn
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 Val Ser Ala Ser Trp Gln Met Thr Ser Pro Ser His Gly Gly Gln Thr
 580 585 590
 Gln Gln Val Gly Val Asn Gly Glu Ala Phe Ser Gln Gln Leu Asp Trp
 595 600 605
 Glu Val Arg Gln Ser Tyr Arg Ala Asp Ala Pro Pro Gly Gly Gly Asn
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 Asn Ser Ala Leu His Leu Ala Trp Asn Gly Asp Tyr Gly Leu Leu Gly
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 Gly Asp Tyr Ser Tyr Ser Arg Ala Met Arg Gln Met Gly Val Asn Ile
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 675 680 685
 Pro Val Gly Gly Trp Pro Gly Val Lys Thr Asp Phe Arg Gly Asp Thr
 690 695 700
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Lys Gly Glu Leu Thr Val Lys Trp Gly Ala Gln Gln Cys Arg Val Asn
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<211> 156

<212> PRT

<213> Salmonella typhimurium

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35 40 45

Val Pro Asp Gly Met Val Leu Ala Gln Gly Trp Val Thr Tyr His Gly
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Ser His Ser Gly Phe Arg Val Trp Ser Asp Glu Gln Lys Ala Gly Asn
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Thr Pro Thr Val Leu Leu Leu Ser Gly Gln Gln Asp Pro Arg His His
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Ile Gln Val Arg Leu Glu Gly Glu Gly Trp Gln Pro Asp Thr Val Ser
100 105 110

Gly Arg Gly Ala Ile Leu Arg Thr Ala Ala Asp Asn Ala Ser Phe Ser
115 120 125

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SEQUENCE LISTING NO. 2

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<120> The complete sequence of the tcf insert of Salmonella enterica serovar Typhi.

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<160> 6

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<223> tcfC putative fimbrial subunit

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<222> (6052)..(7131)

<223> tcfD putative fimbrial subunit

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<222> (7264)..(7719)

<223> tinR putative transcriptional regulator

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cgc gaa gag gcc acc tcg ctg ttc gtc tat tct aaa tca gat cat gtg 2059
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 Gln Tyr Ile Arg Thr Arg Ile Met Arg Ile Glu His Pro Gly Met Pro
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 75 80 85

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 Val Ser Pro Glu Lys Phe Ala Leu Ser Pro Gly Thr Lys Lys Thr Ile
 90 95 100

cgt gtt atc agt act cag gca ccg gaa aga gag gaa gcc tgg cgg gta 2251
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 Tyr Phe Glu Ala Val Pro Glu Leu Glu Asp Asp Pro Gln Ala Gly Gly
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 170 175 180

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 Pro Gly Gly Ser Ala Asp Ile Pro Ala Gly Ile Lys Ser Asn Ala Phe
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 215 220 225 230

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 Leu Thr Ala Ala Gly Lys
 235

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 240 245

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Ala Ala Ala Val Ala Leu Ala Thr Val Tyr Ser Phe Ser Val Ser Ala			
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ggt cag aag gat att acc gtc act gcc aat att gac agt aca ctt gaa			2835
Val Gln Lys Asp Ile Thr Val Thr Ala Asn Ile Asp Ser Thr Leu Glu			
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ctg ctg cag gcc gat ggt tca tcc ctc ccg tct act atg aag ctg gat			2883
Leu Leu Gln Ala Asp Gly Ser Ser Leu Pro Ser Thr Met Lys Leu Asp			
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ttc atg ccg ggt aag ggc ctg gtc cat aaa tca ctc cag acc cgc ctt			2931
Phe Met Pro Gly Lys Gly Leu Val His Lys Ser Leu Gln Thr Arg Leu			
	315	320	325
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Tyr Ser Asn Asp Gln Thr Lys Ser Val Asn Val Lys Leu Leu Asn Ala			
	330	335	340
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Pro Gln Leu Ile Asn Val Leu Asp Pro Thr Lys Thr Ile Asp Met Glu			
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Leu Asn Leu Asp Ile Gly Gln Lys Ala Gly Ala Ala Leu Gln Asn Leu			
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cct gcc ggt gaa tac agc gga ttg gtc agt ctg gtg att tca cag gct			3219
Pro Ala Gly Glu Tyr Ser Gly Leu Val Ser Leu Val Ile Ser Gln Ala			
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gtc act gcc ggc taa taactgggta ttagctcttc atctgatccg gttttggggg			3274
Val Thr Ala Gly			
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ctg gaa gga cag act gag caa att gaa gtg ttg cta cca ggg cat tca			3482
Leu Glu Gly Gln Thr Glu Gln Ile Glu Val Leu Leu Pro Gly His Ser			
	455	460	465
			470

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Ser Pro Leu Met Val Leu Glu Ser Ser Gly Leu Ala Ala Leu Pro Ala	
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Asn Ser Asn Leu Val Cys Gly Val Ser Glu Ala Lys Asp Ser Ser Glu	
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Cys Gly Tyr Val Ala Thr Asp Lys Glu Asp Val Ala Val Ile Phe Asp	
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Glu Asn Asn Ala Gln Leu Ser Leu Phe Leu Asn Arg Asp Trp Leu Pro	
555 560 565	
gat gaa gaa cga cgt gat aaa cgc tgg ctg act ccg acc ccg gag ggt	3818
Asp Glu Glu Arg Arg Asp Lys Arg Trp Leu Thr Pro Thr Pro Glu Gly	
570 575 580	
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Val Ser Ala Phe Ile His Arg Gln Thr Leu Tyr Leu Ser Asp Asp Leu	
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His Ser Arg Asn Met Thr Leu Asn Gly Ser Gly Ala Leu Gly Leu Gly	
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Gln Asp Leu Gly Asn Gln Tyr Tyr Leu Gln Ala Gly Arg Met Asp Gln	
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Arg Asn Leu Ser Ser Ala Thr Gly Gly Asp Phe Gly Phe Ser Leu Leu	
665 670 675	
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Pro Leu Ser Arg Phe Asp Gly Leu Arg Thr Gly Thr Thr Gln Ala Tyr	
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Val Asn His Glu Val Asp His Asn Ala Thr Pro Val Met Val Gln Val	
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acc cga aat gcc cgt att gat att tat cgt ggc agc gag ttg ctg ggg	4250
Thr Arg Asn Ala Arg Ile Asp Ile Tyr Arg Gly Ser Glu Leu Leu Gly	
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Pro Pro Gly Ser Tyr Pro Leu Ala Leu Arg Val Tyr Glu Asp Gly Ile	
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Val Leu Asp Gly Thr Leu Asp Leu Ser Ala Gly Ile Leu His Gly Thr	
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Ser Ala Ser Leu Trp Arg Asn His Thr Glu Ser Asp Ala Cys Ser Gly	
875 880 885	
cgt cat cca cag tca gtg cat gcc agt atg acc tgc cag act tcg atg	4778
Arg His Pro Gln Ser Val His Ala Ser Met Thr Cys Gln Thr Ser Met	
890 895 900	
aac gcc tcc ctg tcg gtt tcg gtg ggg aac tgg tat gcc cta ctg gga	4826
Asn Ala Ser Leu Ser Val Ser Val Gly Asn Trp Tyr Ala Leu Leu Gly	
905 910 915	
tac agt acc agc agg aca gaa ggt cgg ccg gtt tac cgg gga tat gat	4874
Tyr Ser Thr Ser Arg Thr Glu Gly Arg Pro Val Tyr Arg Gly Tyr Asp	
920 925 930	
gat aac agt gac aaa gaa aat gtg ttc tgg cga cag gca tac atc cct	4922
Asp Asn Ser Asp Lys Glu Asn Val Phe Trp Arg Gln Ala Tyr Ile Pro	
935 940 945 950	

gcc tct cac cgc gaa tct gct cag gct agt gca acg tac agc ctt aat	4970
Ala Ser His Arg Glu Ser Ala Gln Ala Ser Ala Thr Tyr Ser Leu Asn	
955 960 965	
atg gct ggc atg aat att aat acc cat ggg gga gta tgg cga acc cga	5018
Met Ala Gly Met Asn Ile Asn Thr His Gly Gly Val Trp Arg Thr Arg	
970 975 980	
aat gac gga gtg aat gat gat ggc ttg ttt atg agt gtc agt gtg tca	5066
Asn Asp Gly Val Asn Asp Asp Gly Leu Phe Met Ser Val Ser Val Ser	
985 990 995	
tat gcc tct caa cca ccg aca atg act ggc agt aat agg tat acc tca	5114
Tyr Ala Ser Gln Pro Pro Thr Met Thr Gly Ser Asn Arg Tyr Thr Ser	
1000 1005 1010	
gcc ggg acc gat att cac agt agc cgg aat caa aaa aca cag acg tcc	5162
Ala Gly Thr Asp Ile His Ser Ser Arg Asn Gln Lys Thr Gln Thr Ser	
1015 1020 1025 1030	
tgg aat gtg aac cat gtg aga tcc tgg cag cag gat ctg tat cgt gaa	5210
Trp Asn Val Asn His Val Arg Ser Trp Gln Gln Asp Leu Tyr Arg Glu	
1035 1040 1045	
ctg tcg gtg ggt ttc tcc ggt tat aac gac gac agc tgg agc ggg agt	5258
Leu Ser Val Gly Phe Ser Gly Tyr Asn Asp Asp Ser Trp Ser Gly Ser	
1050 1055 1060	
ctc ggc gga cgc atg agc ggc cgt atg ggt gaa ctg agc gcc act atc	5306
Leu Gly Gly Arg Met Ser Gly Arg Met Gly Glu Leu Ser Ala Thr Ile	
1065 1070 1075	
agt aac tcc cat caa cgt aat gcg ggc agc gcc agt tca ctc acc gct	5354
Ser Asn Ser His Gln Arg Asn Ala Gly Ser Ala Ser Ser Leu Thr Ala	
1080 1085 1090	
ggc tac agc tcg tct ctg gcg tta tcc cgt aat gga ctg ttc tgg gga	5402
Gly Tyr Ser Ser Ser Leu Ala Leu Ser Arg Asn Gly Leu Phe Trp Gly	
1095 1100 1105 1110	
ggt ggt cag gac ggt gaa ccg gcc tct ggc atg gcg gtg aac gtg gag	5450
Gly Gly Gln Asp Gly Glu Pro Ala Ser Gly Met Ala Val Asn Val Glu	
1115 1120 1125	
tca gag ggg gac gag ggc agt agc ggg aaa gta gtc agc gtt cgt ggc	5498
Ser Glu Gly Asp Glu Gly Ser Ser Gly Lys Val Val Ser Val Arg Gly	
1130 1135 1140	
agc agc cag ccg ttc agt ctc ggt ttt ggt cag cag tcg ctg ttg ctg	5546
Ser Ser Gln Pro Phe Ser Leu Gly Phe Gly Gln Gln Ser Leu Leu Leu	
1145 1150 1155	
atg gaa ggc tat aac gcc acg gag gtg acc att gag gat gca ggg gtt	5594
Met Glu Gly Tyr Asn Ala Thr Glu Val Thr Ile Glu Asp Ala Gly Val	
1160 1165 1170	
agt tca cag ggt atg gca ggc gta aaa gcg gga ggg gga agc agg tgt	5642
Ser Ser Gln Gly Met Ala Gly Val Lys Ala Gly Gly Gly Ser Arg Cys	

1175	1180	1185	1190	
tac ttc ctg aca ccc ggg cat ctg ctg gtt cac aac atc agc gcc agt				5690
Tyr Phe Leu Thr Pro Gly His Leu Leu Val His Asn Ile Ser Ala Ser				
1195	1200	1205		
atg agc cga ctg tac gtt ggc cgc gta ctg gac aag gat ggc aga ccg				5738
Met Ser Arg Leu Tyr Val Gly Arg Val Leu Asp Lys Asp Gly Arg Pro				
1210	1215	1220		
ctg ctg gac gca cag cca ctg aac tat cca ttt ttg tgc ttg gga cct				5786
Leu Leu Asp Ala Gln Pro Leu Asn Tyr Pro Phe Leu Ser Leu Gly Pro				
1225	1230	1235		
tcc ggg cga ttt agc ctg cag agc gag cat aaa gaa tcc agc ctg tgg				5834
Ser Gly Arg Phe Ser Leu Gln Ser Glu His Lys Glu Ser Ser Leu Trp				
1240	1245	1250		
ctg ctg tct aaa aac agg atc ctg cgt tgt ccg atg tca gta cat aaa				5882
Leu Leu Ser Lys Asn Arg Ile Leu Arg Cys Pro Met Ser Val His Lys				
1255	1260	1265	1270	
cgt cgg gat gtt atg cag gta gtg ggt gat gtg cgg tgt gaa tta agt				5930
Arg Arg Asp Val Met Gln Val Val Gly Asp Val Arg Cys Glu Leu Ser				
1275	1280	1285		
gac gtg gat gcc ctg cca cag gcg ttg caa ata tgc ccg cgg gtc atc				5978
Asp Val Asp Ala Leu Pro Gln Ala Leu Gln Ile Ser Pro Arg Val Ile				
1290	1295	1300		
cgt ttg ctg aac gtg gca ggt ttg ctg cgc cat tcc gtt cag gaa gcc				6026
Arg Leu Leu Asn Val Ala Gly Leu Leu Arg His Ser Val Gln Glu Ala				
1305	1310	1315		
tga cgtagagata aaggcggttaa ct atg agt aat aaa atg aag tgg acg agt				6078
Met Ser Asn Lys Met Lys Trp Thr Ser				
1320	1325			
atg aca gcc cat tgg tca gca att att aat ttc atc cga aaa tat gtt				6126
Met Thr Ala His Trp Ser Ala Ile Ile Asn Phe Ile Arg Lys Tyr Val				
1330	1335	1340		
tat cca gca agg ata att gcc atc ctg ctg atg gct ggc gct aca ctg				6174
Tyr Pro Ala Arg Ile Ile Ala Ile Leu Leu Met Ala Gly Ala Thr Leu				
1345	1350	1355	1360	
cca caa gtc gcc gat gcg att acc gtc gac ctg aat tac gac aag aac				6222
Pro Gln Val Ala Asp Ala Ile Thr Val Asp Leu Asn Tyr Asp Lys Asn				
1365	1370	1375		
aat gta gcg gtc atc act cct gtc tgg tcc caa gaa tgg agt gta gca				6270
Asn Val Ala Val Ile Thr Pro Val Trp Ser Gln Glu Trp Ser Val Ala				
1380	1385	1390		
aat gtg ttg ggg gga tgg gta tgt cgt tca aac agg aat gaa aat gag				6318
Asn Val Leu Gly Gly Trp Val Cys Arg Ser Asn Arg Asn Glu Asn Glu				
1395	1400	1405		
ggg gcg tgt gaa gaa aca cat ttg gta tgg tgg tat gct ttt gga gct				6366
Gly Ala Cys Glu Glu Thr His Leu Val Trp Trp Tyr Ala Phe Gly Ala				

1410	1415	1420	
tat tca aaa att cgt ctg cgt ttc aga gaa caa atc agc cat gcc gaa Tyr Ser Lys Ile Arg Leu Arg Phe Arg Glu Gln Ile Ser His Ala Glu 1425	1430	1435	1440 6414
att acg ctc ata ctg ctc ggc agt gtt cgt gat gcc tgt tat act ggt Ile Thr Leu Ile Leu Leu Gly Ser Val Arg Asp Ala Cys Tyr Thr Gly 1445	1450	1455	6462
gtc atc aac atg aac gct gct gca tgt caa tgg ggt agg tgc ctg aaa Val Ile Asn Met Asn Ala Ala Ala Cys Gln Trp Gly Arg Ser Leu Lys 1460	1465	1470	6510
ctt agg ata cct tca gaa gag ctt gcg aag ata cct aca agc gga aca Leu Arg Ile Pro Ser Glu Glu Leu Ala Lys Ile Pro Thr Ser Gly Thr 1475	1480	1485	6558
tgg aaa gca acg tta gtc ctg gat tat tta caa tgg ggc gga gac gat Trp Lys Ala Thr Leu Val Leu Asp Tyr Leu Gln Trp Gly Gly Asp Asp 1490	1495	1500	6606
cct tta ggc aca tca act aca gat atc acg ctg aat gta aca gac cac Pro Leu Gly Thr Ser Thr Thr Asp Ile Thr Leu Asn Val Thr Asp His 1505	1510	1515	1520 6654
ttt gct gaa aat gcg gct att tac ttt ccg caa ttt ggt aca gca acg Phe Ala Glu Asn Ala Ala Ile Tyr Phe Pro Gln Phe Gly Thr Ala Thr 1525	1530	1535	6702
ccc cgg gtg gac ctg aat ctt cac cgg atg aat gcc tca caa atg tgc Pro Arg Val Asp Leu Asn Leu His Arg Met Asn Ala Ser Gln Met Ser 1540	1545	1550	6750
ggc agg gct aat ctg gat atg tgt ctg tat gac gga ggt gtg aaa gcc Gly Arg Ala Asn Leu Asp Met Cys Leu Tyr Asp Gly Gly Val Lys Ala 1555	1560	1565	6798
cgt tca tta cag atg aag ata gaa gga agc aat aag tca ggt acg gga Arg Ser Leu Gln Met Lys Ile Glu Gly Ser Asn Lys Ser Gly Thr Gly 1570	1575	1580	6846
ttt cag gtt ata aag agc gat tct gct gat acg att gat tat gcg gtc Phe Gln Val Ile Lys Ser Asp Ser Ala Asp Thr Ile Asp Tyr Ala Val 1585	1590	1595	1600 6894
agt atg aat tat ggg gga cga agt att cct gtc acc cgt ggc gtg gag Ser Met Asn Tyr Gly Gly Arg Ser Ile Pro Val Thr Arg Gly Val Glu 1605	1610	1615	6942
ttc agt ctg gat aac gtg gat aaa gca gca acg cgt ccg gtg gta ctt Phe Ser Leu Asp Asn Val Asp Lys Ala Ala Thr Arg Pro Val Val Leu 1620	1625	1630	6990
ccc ggg caa cgg cag gcg gta cgt tgt gtg cca gtg ccc ctt acc ctg Pro Gly Gln Arg Gln Ala Val Arg Cys Val Pro Val Pro Leu Thr Leu 1635	1640	1645	7038

aca aca caa ccc ttt aac atc aga gag aag cgt tct ggt gag tat cag 7086
 Thr Thr Gln Pro Phe Asn Ile Arg Glu Lys Arg Ser Gly Glu Tyr Gln
 1650 1655 1660

gga acg ctg aca gtg aca atg ctg atg gga aca caa acc ccc tga 7131
 Gly Thr Leu Thr Val Thr Met Leu Met Gly Thr Gln Thr Pro
 1665 1670 1675

cagtaattat ttattttatt gatattcttc ttatatggtt ttttaaatca gagttctctt 7191
 tatatacttg ttttatttaa taaagagaat ctattcactt atgaaaatca atgcgtgagg 7251
 ttctgctttc ct atg act gtg tat tta gat gat aaa gat aaa gaa tta ttg 7302
 Met Thr Val Tyr Leu Asp Asp Lys Asp Lys Glu Leu Leu
 1680 1685 1690

aaa gaa atc caa aaa gat tgt gca caa act tta tgg caa ctt gca tat 7350
 Lys Glu Ile Gln Lys Asp Cys Ala Gln Thr Leu Trp Gln Leu Ala Tyr
 1695 1700 1705

aaa gtg gga ctt acg ccc aca cca tgt ttc aaa cgt tta aaa aaa ctt 7398
 Lys Val Gly Leu Thr Pro Thr Pro Cys Phe Lys Arg Leu Lys Lys Leu
 1710 1715 1720

aaa gac agg ggg gtt atc att ggt cag ttc gct tta ttg gat aag gaa 7446
 Lys Asp Arg Gly Val Ile Ile Gly Gln Phe Ala Leu Leu Asp Lys Glu
 1725 1730 1735 1740

aaa cta ggt ctt tca ctt aat gtc ttt att atg att aac ata tct gag 7494
 Lys Leu Gly Leu Ser Leu Asn Val Phe Ile Met Ile Asn Ile Ser Glu
 1745 1750 1755

gag caa tac gct agt att tct gag aaa ata aag tca atg cct gag gtt 7542
 Glu Gln Tyr Ala Ser Ile Ser Glu Lys Ile Lys Ser Met Pro Glu Val
 1760 1765 1770

att gcc ttt tat cga att tct gga tca ttt aat tat tta atg cat aca 7590
 Ile Ala Phe Tyr Arg Ile Ser Gly Ser Phe Asn Tyr Leu Met His Thr
 1775 1780 1785

gta ttt aca gat atg aac gat tac tat agt ttt tat gag aaa ata ata 7638
 Val Phe Thr Asp Met Asn Asp Tyr Tyr Ser Phe Tyr Glu Lys Ile Ile
 1790 1795 1800

tta act aat tct tca att agt gga tct gca tcg agc ttt gtt ctt gag 7686
 Leu Thr Asn Ser Ser Ile Ser Gly Ser Ala Ser Ser Phe Val Leu Glu
 1805 1810 1815 1820

caa ata aag gaa aca aac gaa ctg tca gtg tga aagtgtgatg tgtacttact 7739
 Gln Ile Lys Glu Thr Asn Glu Leu Ser Val
 1825 1830

gatttaatac attattatcc ttcttacgga acaacaacgg cagattgcgg ctggtgaaca 7799
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<210> 2

<211> 236

<212> PRT

<213> Salmonella typhi

<400> 2

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Phe	Ala	Cys	Gly	His	Ala	Arg	Ala	Asn	Met	Leu	Val	Tyr	Pro	Met	Ala
	20							25						30	

Ala	Glu	Ile	Asn	Ser	Ser	Arg	Glu	Glu	Ala	Thr	Ser	Leu	Phe	Val	Tyr
	35						40					45			

Ser Lys Ser Asp His Val Gln Tyr Ile Arg Thr Arg Ile Met Arg Ile
 50 55 60
 Glu His Pro Gly Met Pro Gln Glu Lys Glu Val Pro Ala Gly Asn Asp
 65 70 75 80
 Ile Glu Thr Gly Leu Val Val Ser Pro Glu Lys Phe Ala Leu Ser Pro
 85 90 95
 Gly Thr Lys Lys Thr Ile Arg Val Ile Ser Thr Gln Ala Pro Glu Arg
 100 105 110
 Glu Glu Ala Trp Arg Val Tyr Phe Glu Ala Val Pro Glu Leu Glu Asp
 115 120 125
 Asp Pro Gln Ala Gly Gly Lys Gln Asn Ser Ser Val Ser Val Asn Leu
 130 135 140
 Val Trp Gly Val Leu Leu Arg Val Ser Pro Ser Asp Pro Arg Pro Ala
 145 150 155 160
 Leu Val Thr Asp Gly His His Leu Leu Asn Thr Gly Asn Thr Arg Leu
 165 170 175
 Ser Leu Ile Arg Ala Gly Asn Cys Asp Thr Thr Cys His Trp Gln Asn
 180 185 190
 Ile Gly Lys Ser Ile Tyr Pro Gly Gly Ser Ala Asp Ile Pro Ala Gly
 195 200 205
 Ile Lys Ser Asn Ala Phe Arg Val Glu Tyr Arg Thr Gly Ala Asn Ser
 210 215 220
 Pro Val Ile Ser Ala Asp Leu Thr Ala Ala Gly Lys
 225 230 235

<210> 3
 <211> 191
 <212> PRT
 <213> Salmonella typhi

<400> 3
 Met Tyr Thr Glu Cys Thr Tyr Ile Thr Val Ile Asn Asn Lys Ala Arg
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 Leu Phe Phe Met Asn Met Lys Thr Ser Phe Ile Ala Ala Ala Val Ala
 20 25 30
 Leu Ala Thr Val Tyr Ser Phe Ser Val Ser Ala Val Gln Lys Asp Ile
 35 40 45
 Thr Val Thr Ala Asn Ile Asp Ser Thr Leu Glu Leu Leu Gln Ala Asp
 50 55 60
 Gly Ser Ser Leu Pro Ser Thr Met Lys Leu Asp Phe Met Pro Gly Lys
 65 70 75 80
 Gly Leu Val His Lys Ser Leu Gln Thr Arg Leu Tyr Ser Asn Asp Gln
 85 90 95

Thr Lys Ser Val Asn Val Lys Leu Leu Asn Ala Pro Gln Leu Ile Asn
 100 105 110

Val Leu Asp Pro Thr Lys Thr Ile Asp Met Glu Val Thr Leu Gly Gly
 115 120 125

Arg Ser Leu Thr Thr Thr Asn Ser Val Leu Glu Ala Lys Thr Leu Phe
 130 135 140

Pro Asp Gly Lys Thr Gly Asp Ala Ser Ala Leu Leu Asn Leu Asp Ile
 145 150 155 160

Gly Gln Lys Ala Gly Ala Ala Leu Gln Asn Leu Pro Ala Gly Glu Tyr
 165 170 175

Ser Gly Leu Val Ser Leu Val Ile Ser Gln Ala Val Thr Ala Gly
 180 185 190

<210> 4
 <211> 889
 <212> PRT
 <213> Salmonella typhi

<400> 4
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Ile Pro Pro Pro Gly Phe Glu Ser Leu Leu Glu Gly Gln Thr Glu Gln
 20 25 30

Ile Glu Val Leu Leu Pro Gly His Ser Leu Gly Leu Phe Pro Val Val
 35 40 45

Val Lys Pro Asp Thr Val Gln Phe Met Ser Pro Leu Met Val Leu Glu
 50 55 60

Ser Ser Gly Leu Ala Ala Leu Pro Ala Ala Glu Arg Gln Lys Ala Leu
 65 70 75 80

Ala Ala Leu Ser Arg Pro Leu Leu Arg Asn Ser Asn Leu Val Cys Gly
 85 90 95

Val Ser Glu Ala Lys Asp Ser Ser Glu Cys Gly Tyr Val Ala Thr Asp
 100 105 110

Lys Glu Asp Val Ala Val Ile Phe Asp Glu Asn Asn Ala Gln Leu Ser
 115 120 125

Leu Phe Leu Asn Arg Asp Trp Leu Pro Asp Glu Glu Arg Arg Asp Lys
 130 135 140

Arg Trp Leu Thr Pro Thr Pro Glu Gly Val Ser Ala Phe Ile His Arg
 145 150 155 160

Gln Thr Leu Tyr Leu Ser Asp Asp Leu His Ser Arg Asn Met Thr Leu
 165 170 175

Asn Gly Ser Gly Ala Leu Gly Leu Gly Asp Gly Arg Tyr Leu Gly Gly
 180 185 190
 Asp Trp Ala Ala Ile Trp Asn Gln Ser Glu His Tyr Asn Asn Ser Gln
 195 200 205
 Ala Trp Phe Asp Asn Leu Phe Val Arg Gln Asp Leu Gly Asn Gln Tyr
 210 215 220
 Tyr Leu Gln Ala Gly Arg Met Asp Gln Arg Asn Leu Ser Ser Ala Thr
 225 230 235 240
 Gly Gly Asp Phe Gly Phe Ser Leu Leu Pro Leu Ser Arg Phe Asp Gly
 245 250 255
 Leu Arg Thr Gly Thr Thr Gln Ala Tyr Val Asn His Glu Val Asp His
 260 265 270
 Asn Ala Thr Pro Val Met Val Gln Val Thr Arg Asn Ala Arg Ile Asp
 275 280 285
 Ile Tyr Arg Gly Ser Glu Leu Leu Gly Ser Gln Phe Leu Thr Pro Gly
 290 295 300
 Met His Thr Leu Asp Thr His Ser Leu Pro Pro Gly Ser Tyr Pro Leu
 305 310 315 320
 Ala Leu Arg Val Tyr Glu Asp Gly Ile Leu Arg Arg Thr Glu Thr Gln
 325 330 335
 Pro Phe Ser Lys Gly Gly Asn Ser Phe Ser Ala Gln Thr Gln Trp Phe
 340 345 350
 Ile Gln Gly Gly Leu Glu Asp Thr Gly Asp Lys Ala Ser His Tyr Asp
 355 360 365
 Gly Glu Thr Val Met Ala Ala Gly Phe Gln Thr Gly Leu Arg Lys Asn
 370 375 380
 Ile Ser Leu Thr Glu Gly Ile Ser Leu Ala His Glu Ala Trp Tyr Ser
 385 390 395 400
 Glu Thr Arg Leu Asn Ser Gln His Ala Val Leu Asp Gly Thr Leu Asp
 405 410 415
 Leu Ser Ala Gly Ile Leu His Gly Thr Asp Ser Thr Ser Gly Asn Thr
 420 425 430
 Glu Gln Val Thr Tyr Asn Asp Gly Phe Ser Ala Ser Leu Trp Arg Asn
 435 440 445
 His Thr Glu Ser Asp Ala Cys Ser Gly Arg His Pro Gln Ser Val His
 450 455 460
 Ala Ser Met Thr Cys Gln Thr Ser Met Asn Ala Ser Leu Ser Val Ser
 465 470 475 480
 Val Gly Asn Trp Tyr Ala Leu Leu Gly Tyr Ser Thr Ser Arg Thr Glu
 485 490 495

Gly Arg Pro Val Tyr Arg Gly Tyr Asp Asp Asn Ser Asp Lys Glu Asn
 500 505 510
 Val Phe Trp Arg Gln Ala Tyr Ile Pro Ala Ser His Arg Glu Ser Ala
 515 520 525
 Gln Ala Ser Ala Thr Tyr Ser Leu Asn Met Ala Gly Met Asn Ile Asn
 530 535 540
 Thr His Gly Gly Val Trp Arg Thr Arg Asn Asp Gly Val Asn Asp Asp
 545 550 555 560
 Gly Leu Phe Met Ser Val Ser Val Ser Tyr Ala Ser Gln Pro Pro Thr
 565 570 575
 Met Thr Gly Ser Asn Arg Tyr Thr Ser Ala Gly Thr Asp Ile His Ser
 580 585 590
 Ser Arg Asn Gln Lys Thr Gln Thr Ser Trp Asn Val Asn His Val Arg
 595 600 605
 Ser Trp Gln Gln Asp Leu Tyr Arg Glu Leu Ser Val Gly Phe Ser Gly
 610 615 620
 Tyr Asn Asp Asp Ser Trp Ser Gly Ser Leu Gly Gly Arg Met Ser Gly
 625 630 635 640
 Arg Met Gly Glu Leu Ser Ala Thr Ile Ser Asn Ser His Gln Arg Asn
 645 650 655
 Ala Gly Ser Ala Ser Ser Leu Thr Ala Gly Tyr Ser Ser Ser Leu Ala
 660 665 670
 Leu Ser Arg Asn Gly Leu Phe Trp Gly Gly Gly Gln Asp Gly Glu Pro
 675 680 685
 Ala Ser Gly Met Ala Val Asn Val Glu Ser Glu Gly Asp Glu Gly Ser
 690 695 700
 Ser Gly Lys Val Val Ser Val Arg Gly Ser Ser Gln Pro Phe Ser Leu
 705 710 715 720
 Gly Phe Gly Gln Gln Ser Leu Leu Leu Met Glu Gly Tyr Asn Ala Thr
 725 730 735
 Glu Val Thr Ile Glu Asp Ala Gly Val Ser Ser Gln Gly Met Ala Gly
 740 745 750
 Val Lys Ala Gly Gly Gly Ser Arg Cys Tyr Phe Leu Thr Pro Gly His
 755 760 765
 Leu Leu Val His Asn Ile Ser Ala Ser Met Ser Arg Leu Tyr Val Gly
 770 775 780
 Arg Val Leu Asp Lys Asp Gly Arg Pro Leu Leu Asp Ala Gln Pro Leu
 785 790 795 800
 Asn Tyr Pro Phe Leu Ser Leu Gly Pro Ser Gly Arg Phe Ser Leu Gln
 805 810 815

Ser Glu His Lys Glu Ser Ser Leu Trp Leu Leu Ser Lys Asn Arg Ile
820 825 830

Leu Arg Cys Pro Met Ser Val His Lys Arg Arg Asp Val Met Gln Val
835 840 845

Val Gly Asp Val Arg Cys Glu Leu Ser Asp Val Asp Ala Leu Pro Gln
850 855 860

Ala Leu Gln Ile Ser Pro Arg Val Ile Arg Leu Leu Asn Val Ala Gly
865 870 875 880

Leu Leu Arg His Ser Val Gln Glu Ala
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<210> 5

<211> 359

<212> PRT

<213> Salmonella typhi

<400> 5

Met Ser Asn Lys Met Lys Trp Thr Ser Met Thr Ala His Trp Ser Ala
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Ile Ile Asn Phe Ile Arg Lys Tyr Val Tyr Pro Ala Arg Ile Ile Ala
20 25 30

Ile Leu Leu Met Ala Gly Ala Thr Leu Pro Gln Val Ala Asp Ala Ile
35 40 45

Thr Val Asp Leu Asn Tyr Asp Lys Asn Asn Val Ala Val Ile Thr Pro
50 55 60

Val Trp Ser Gln Glu Trp Ser Val Ala Asn Val Leu Gly Gly Trp Val
65 70 75 80

Cys Arg Ser Asn Arg Asn Glu Asn Glu Gly Ala Cys Glu Glu Thr His
85 90 95

Leu Val Trp Trp Tyr Ala Phe Gly Ala Tyr Ser Lys Ile Arg Leu Arg
100 105 110

Phe Arg Glu Gln Ile Ser His Ala Glu Ile Thr Leu Ile Leu Leu Gly
115 120 125

Ser Val Arg Asp Ala Cys Tyr Thr Gly Val Ile Asn Met Asn Ala Ala
130 135 140

Ala Cys Gln Trp Gly Arg Ser Leu Lys Leu Arg Ile Pro Ser Glu Glu
145 150 155 160

Leu Ala Lys Ile Pro Thr Ser Gly Thr Trp Lys Ala Thr Leu Val Leu
165 170 175

Asp Tyr Leu Gln Trp Gly Gly Asp Asp Pro Leu Gly Thr Ser Thr Thr
180 185 190

Asp Ile Thr Leu Asn Val Thr Asp His Phe Ala Glu Asn Ala Ala Ile
195 200 205

Tyr Phe Pro Gln Phe Gly Thr Ala Thr Pro Arg Val Asp Leu Asn Leu
210 215 220

His Arg Met Asn Ala Ser Gln Met Ser Gly Arg Ala Asn Leu Asp Met
225 230 235 240

Cys Leu Tyr Asp Gly Gly Val Lys Ala Arg Ser Leu Gln Met Lys Ile
245 250 255

Glu Gly Ser Asn Lys Ser Gly Thr Gly Phe Gln Val Ile Lys Ser Asp
260 265 270

Ser Ala Asp Thr Ile Asp Tyr Ala Val Ser Met Asn Tyr Gly Gly Arg
275 280 285

Ser Ile Pro Val Thr Arg Gly Val Glu Phe Ser Leu Asp Asn Val Asp
290 295 300

Lys Ala Ala Thr Arg Pro Val Val Leu Pro Gly Gln Arg Gln Ala Val
305 310 315 320

Arg Cys Val Pro Val Pro Leu Thr Leu Thr Thr Gln Pro Phe Asn Ile
325 330 335

Arg Glu Lys Arg Ser Gly Glu Tyr Gln Gly Thr Leu Thr Val Thr Met
340 345 350

Leu Met Gly Thr Gln Thr Pro
355

<210> 6

<211> 151

<212> PRT

<213> Salmonella typhi

<400> 6

Met Thr Val Tyr Leu Asp Asp Lys Asp Lys Glu Leu Leu Lys Glu Ile
1 5 10 15

Gln Lys Asp Cys Ala Gln Thr Leu Trp Gln Leu Ala Tyr Lys Val Gly
20 25 30

Leu Thr Pro Thr Pro Cys Phe Lys Arg Leu Lys Lys Leu Lys Asp Arg
35 40 45

Gly Val Ile Ile Gly Gln Phe Ala Leu Leu Asp Lys Glu Lys Leu Gly
50 55 60

Leu Ser Leu Asn Val Phe Ile Met Ile Asn Ile Ser Glu Glu Gln Tyr
65 70 75 80

Ala Ser Ile Ser Glu Lys Ile Lys Ser Met Pro Glu Val Ile Ala Phe
85 90 95

Tyr Arg Ile Ser Gly Ser Phe Asn Tyr Leu Met His Thr Val Phe Thr
100 105 110

Asp Met Asn Asp Tyr Tyr Ser Phe Tyr Glu Lys Ile Ile Leu Thr Asn
115 120 125

Ser Ser Ile Ser Gly Ser Ala Ser Ser Phe Val Leu Glu Gln Ile Lys
130 135 140

Glu Thr Asn Glu Leu Ser Val
145 150

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